

SEQUENCE LISTING

<110> UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.

<120> DNA SEQUENCE AND EXPRESSED RECOMBINANT GLYCOPROTEINS
RELATED TO FELINE THYROTROPIN

<130> 235-00540201

<140> PCT/US04/03779

<141> 2004-11-12

<150> 60/534,205

<151> 2004-01-05

<150> 60/519,302

<151> 2003-11-12

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 118

<212> PRT

<213> Felis sp.

<400> 1

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Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala Gly Tyr Cys Met
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Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys Tyr Ala Leu Ser
          35           40           45
Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
          50           55           60
Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
          65           70           75           80
Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
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His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro Gln Lys Ser Asp
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Val Val Gly Val Ser Ile
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<212> PRT

<213> Felis sp.

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Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
35 40 45
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
50 55 60
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
65 70 75 80
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
85 90 95
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
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Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
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Gln Lys Ser Asp Val Val Gly Val Ser Ile
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35 40 45
Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala Thr Cys Cys
50 55 60
Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn Ala Lys Val
65 70 75 80
Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His His Lys Ile
85 90 95

<210> 4

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<212> PRT

<213> Felis sp.

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			20					25					30		
Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe	Ser	Lys
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Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala
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Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro	Lys	Asn
	65				70					75					80
Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr	Lys	Ala
				85					90					95	
Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys	His	Cys
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Thr	Arg	Asp	Ile	Asn	Gly	Lys	Leu	Phe	Leu	Pro	Lys	Tyr	Ala	Leu	Ser
		35					40					45			
Gln	Asp	Val	Cys	Thr	Tyr	Arg	Asp	Phe	Leu	Tyr	Lys	Thr	Val	Glu	Ile
	50					55					60				
Pro	Gly	Cys	Pro	His	His	Val	Thr	Pro	Tyr	Phe	Ser	Tyr	Pro	Val	Ala
	65				70					75					80
Val	Ser	Cys	Lys	Cys	Gly	Lys	Cys	Asn	Thr	Asp	Tyr	Ser	Asp	Cys	Ile
				85					90					95	
His	Glu	Ala	Ile	Lys	Thr	Asn	Asp	Cys	Thr	Lys	Pro	Gln	Lys	Ser	Asp
		100						105					110		
Val	Val	Gly	Val	Ser	Ile	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Ser
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Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro Ser Asp Thr Pro
 130 135 140

Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro
 145 150 155 160

Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro
 165 170 175

Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 180 185 190

Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu
 195 200 205

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His His Lys Ile

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 35 40 45

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60

Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140

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Lys	Ala	Pro	Ser	Ala	Ser	Leu	Pro	Ser	Pro	Thr	Arg	Leu	Pro	Gly	Pro	
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Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Phe	Pro	Asp	Gly	Glu	Phe	Thr	Met	
				165					170					175		
Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe	Ser	Lys	
			180					185					190			
Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	
		195					200					205				
Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro	Lys	Asn	
	210					215					220					
Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr	Lys	Ala	
225					230					235					240	
Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys	His	Cys	
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1				5					10					15		
caa	gcg	atg	tct	ttt	tgt	ttt	cca	act	gag	tat	atg	atg	cat	gtc	gaa	96
Gln	Ala	Met	Ser	Phe	Cys	Phe	Pro	Thr	Glu	Tyr	Met	Met	His	Val	Glu	
			20					25					30			
agg	aaa	gag	tgt	gct	tat	tgc	cta	acc	atc	aac	acc	acc	atc	tgt	gct	144
Arg	Lys	Glu	Cys	Ala	Tyr	Cys	Leu	Thr	Ile	Asn	Thr	Thr	Ile	Cys	Ala	
		35				40						45				
gga	tat	tgt	atg	aca	cgg	gat	atc	aat	ggc	aaa	ctg	ttt	ctt	ccc	aaa	192
Gly	Tyr	Cys	Met	Thr	Arg	Asp	Ile	Asn	Gly	Lys	Leu	Phe	Leu	Pro	Lys	
		50				55					60					

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag	240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys	
65 70 75 80	
act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc	288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser	
85 90 95	
tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat	336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr	
100 105 110	
agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc	384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro	
115 120 125	
cag aag tcc gat gtg gta gga gtt tct atc taa	417
Gln Lys Ser Asp Val Val Gly Val Ser Ile	
130 135	

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accatcaaca ccaccatctg tgctggatat tgtatgacac gggtagtag ttcattctcac	180
ttcttttagc tgaaaattag ataaacctag actcagtcca tttctatcca gaaaggaaat	240
gagataaatc acaacctcat ttcacagacc taacggatcat tggctcctta gaggtagagt	300
ccctagggtta taatatacgg acctactcca tacagttggg acagataatt tttacaatag	360
ttttactccc aaagtttatt taaaccttat cttgttccca cgatcaagga taaaagagag	420
gtgtgtgtgt atgtcatttt tttttgtctc tataggattc agtgtggata tgctgaattg	480
gtattgggga atgggactaa ggaatcctcc cccagtccta tttgtatcta tgggatgtaa	540
gcgaattaac atttttgcttc ctcttctgtg ctccctcag gatataaatg gcaactgtt	600
tcttcccaaa tatgtctctgt cccaagatgt ttgcacctac agagacttcc tgtacaagac	660
tgtagaaaata ccaggatgcc cacaccatgt tactccctat ttctcctacc cggtagctgt	720
aagctgtaaa tgtggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa	780
gacaaatgat tgtaccaaac ccagaagtc cgatgtggta ggagtttcta tctaa	835

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aaggaaaaaca aatactttctc caagtggggt gcccgaattt atcaatgcat gggctgctgc	180
ttctccagag cataccccac tccagcaagg tccaagaaga caatgttggg cccaagaac	240
atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac ggtaatggga	300
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Met Asp Tyr Tyr Arg																	
1 5																	
aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt ctg cat att																	162
Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe Leu His Ile																	
10 15 20																	
ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg tgc cca gaa																	210
Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu																	
25 30 35																	
tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt gcc cca att																	258
Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile																	
40 45 50																	
tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc act cca gca																	306
Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala																	
55 60 65																	
agg tcc aag aag aca atg ttg gtc cca aag aac atc acc tca gaa gcc																	354
Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala																	
70 75 80 85																	
aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta atg gga aat																	402
Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn																	
90 95 100																	
gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act tgc tat cac																	450
Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His																	
105 110 115																	
cac aag att																	459
His Lys Ile																	
120																	

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 <222> (61)..(792)
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caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
 Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20 25 30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
 Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
 Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
 Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
 Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct tcc tca 432
 Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140

aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg ggg ccc 480
 Lys Ala Pro Ser Ala 150 155 160

tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt aca atg	528
Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met	
165 170 175	
cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag	576
Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys	
180 185 190	
ttg ggt gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca	624
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
195 200 205	
tac ccc act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac	672
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
210 215 220	
atc acc tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc	720
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
225 230 235 240	
acg gta atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc	768
Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys	
245 250 255	
agc act tgc tat cac cac aag att	792
Ser Thr Cys Tyr His His Lys Ile	
260	

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accatcaaca ccaccatctg tgctggatat tgtatgacac gggatatgtag ttcatctcac	180
ttcttttagc tgaaaattag ataaacctag actcagtcca tttctatcca gaaaggaaat	240
gagataaatc acaacctcat ttcacagacc taacggtcat tggctcctta gaggtagagt	300
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ttttactccc aaagtttatt taaaccttat cttgttccca cgatcaagga taaaagagag	420
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gtattgggga atgggactaa ggaatcctcc cccagtccta tttgtatcta tgggatgtaa	540
gcgaattaac attttgcttc ctcttctgtg cttccctcag gatatacatg gcaaaactgtt	600
tcttcccaaa tatgctctgt cccaagatgt ttgcacctac agagacttcc tgtacaagac	660
tgtagaaata ccaggatgcc cacaccatgt tactccctat ttctcctacc cggtagctgt	720
aagctgtaaa tgtggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa	780
gacaaatgat tgtaccaaac cccagaagtc cgatgtggta ggagtctcta tccaggactc	840
ctcttctca aaggccctt ccgccagcct tccaagccca acgcgtctcc cggggccctc	900
ggacaccccg atcctccac aatttctga tggagagttt acaatgcagg ggtgcccaga	960
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gggctgctgc ttctccagag cataccccac tccagcaagg tccaagaaga caatgttggt	1080
cccaaagaac atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac	1140
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ccacaagatt	1210

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 tgatggagag 130

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 tgcctaacca tcaacaccac catctgtgct ggatattgta tgacacgggt atgtagtcca 180
 tctcacttct ttttagctgaa aattagataa acctagactc agtccatttc tatccagaaa 240
 ggaaatgaga taaatcacia cctcatttca cagacctaac ggtcattggc tccttagagg 300
 tagagtcctt aggttataat atacggacct actccataca gttggtacag ataattttta 360
 caatagtttt actcccaaag tttattttaa ccttatcttg tccccacgat caaggataaa 420
 agagaggtgt gtgtgtatgt catttttttt tgtctctata ggattcagtg tggatatgct 480
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 caagactgta gaaataccag gatgccaca ccatgttact ccctatttct cctaccgggt 720
 agctgtaagc tgtaaatgtg gcaagtgtaa tactgactat agcgactgca tacatgaggc 780
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 <212> DNA
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 Met Asp
 1
 tac tac aga aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt 165
 Tyr Tyr Arg Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe
 5 10 15
 ctg cat att ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg 213
 Leu His Ile Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly
 20 25 30

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tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt	261
Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly	
35 40 45 50	
gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc	309
Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro	
55 60 65	
act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac atc acc	357
Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr	
70 75 80	
tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta	405
Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val	
85 90 95	
atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act	453
Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr	
100 105 110	
tgc tat cac cac aag att atc gaa ggt cgt gac tac aag gac gat gac	501
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115 120 125 130	
gat aag taagcggccg ctatg	522
Asp Lys	

<210> 16
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<400> 16	
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Val Phe Leu His Ile Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met	
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Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys	
35 40 45	
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
50 55 60	
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
65 70 75 80	
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
85 90 95	
Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys	
100 105 110	
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Asp Asp Asp Lys
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Cys Gly Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His
15 20 25 30

gtc gaa agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc 144
Val Glu Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile
35 40 45

tgt gct gga tat tgt atg aca cgg gtatgtagtt catctcactt cttttagctg 198
Cys Ala Gly Tyr Cys Met Thr Arg
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aaaattagat aaacctagac tcagtcatt tctatccaga aaggaaatga gataaatcac 258

aacctcattt cacagacctt acggtcattg gtccttaga ggtagagtcc ctaggttata 318

atatacggac ctactccata cagttggtag agataatttt tacaatagtt ttactcccaa 378

agttttattta aaccttatct tggtccacg atcaaggata aaagagaggt gtgtgtgtat 438

gtcattttttt ttgtctcta taggattcag tgtggatatg ctgaattggg attggggaat 498

gggactaagg aatcctcccc cagtcctatt tgtatctatg ggatgtaagc gaattaacat 558

tttgcttctt cttctgtgct tccctcag gat atc aat ggc aaa ctg ttt ctt 610
Asp Ile Asn Gly Lys Leu Phe Leu
55 60

ccc aaa tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg 658
Pro Lys Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu
65 70 75

tac aag act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat 706
Tyr Lys Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr
80 85 90

13/14

ttc tcc tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act	754
Phe Ser Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr	
95 100 105 110	
gac tat agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc	802
Asp Tyr Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr	
115 120 125	
aaa ccc cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct	850
Lys Pro Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser	
130 135 140	
tcc tca aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg	898
Ser Ser Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro	
145 150 155	
ggg ccc tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt	946
Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe	
160 165 170	
aca atg cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc	994
Thr Met Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe	
175 180 185 190	
tcc aag ttg ggt gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc	1042
Ser Lys Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser	
195 200 205	
aga gca tac ccc act cca gca agg tcc aag aag aca atg ttg gtc cca	1090
Arg Ala Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro	
210 215 220	
aag aac atc acc tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc	1138
Lys Asn Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr	
225 230 235	
aag gcc acg gta atg gga aat gcc aaa gtg gag aat cac aca gag tgc	1186
Lys Ala Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys	
240 245 250	
cac tgc agc act tgc tat cac cac aag att atc gaa ggt cgt gac tac	1234
His Cys Ser Thr Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr	
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 Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45
 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80
 Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95
 Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110
 Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125
 Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140
 Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
 145 150 155 160
 Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
 165 170 175
 Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
 180 185 190
 Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 195 200 205
 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 210 215 220
 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 225 230 235 240
 Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 245 250 255
 Ser Thr Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp
 260 265 270
 Asp Asp Asp Lys
 275